

Supplementary Data Legends:

Supplementary Data 1: **a**, Proteomics of T1, T2, MZ and FoB cells containing peptide counts, copy numbers per cell and LFQ intensities. **b**, Differentially expressed proteins that are found in all B cell subsets. **c**, Differentially expressed proteins that are unique to T1 and MZ B cells.

Supplementary Data 2: Transcript per million (TPM) and protein copy numbers of genes identified by Illumina RNA-sequencing and proteomics.

Supplementary Data 3: **a**, Early activation genes extracted from DESeq analysis of Garruss et al. (ref. 56). **b**, PC-related genes extracted from DESeq analysis of Gaudette et al. (ref. 16).

Supplementary Data 4: Full-length transcript measured by Oxford Nanopore Technology (ONT) sequencing as in Fig S5b and compared to Illumina sequencing.

Supplementary Data 5: **a**, List of poised mRNAs linked to early activation in B cells. **b**, List of poised mRNAs linked to plasmablast formation and antibody secretion.

Supplementary Data 6: List of antibodies used for flow cytometry analysis.